In The Specification:

Please replace the Sequence Listing (1 page) filed on April 19, 2002 with the substitute Sequence Listing (1 page) filed herewith.

Please replace the paragraph beginning at page 6, line 5, with the following rewritten paragraph:

C2

As used herein, "analyte" refers to any atom and/or molecule; including their complexes and fragment ions. In the case of biological molecules/macromolecules or "biopolymers", such analytes include but are not limited to: proteins, peptides, DNA, RNA, carbohydrates, steroids, and lipids. Note that most important biomolecules under investigation for their involvement in the structure or regulation of life processes are quite large (typically several thousand times larger than H_2O) .

Please replace the paragraph beginning at page 19, line 2, with the following rewritten paragraph:

C3

FIGURE 1 is a representation of derived data which characterizes a disease specific marker having a particular sequence (SEQ ID NO:1) useful in evidencing and categorizing at least one particular disease state[;]. The patients listed in the data table show the presence of the disease specific marker (SEQ ID NO:1) in their serum.

Please replace the paragraph beginning at page 19, line 6, with the following rewritten paragraph:

C4 FIGURE 2 is the characteristic profile derived via SELDI/TOF MS of the disease specific marker of Figure 1. SEQ ID NO:1 is shown.

Please replace the paragraph beginning at page 22, line 19, with the following re-written paragraph:

C5 **Chelating [Sepharose] SEPHAROSE Mini Column**

1. Dilute Sera in Sample/Running buffer;

2. Add Chelating [Sepharose] SEPHAROSE slurry to column and allow column to pack;

3. Add UF water to the column to aid in packing;

4. Add Charging Buffer once water is at the level of the resin surface;

5. Add UF water to wash through non bound metal ions once charge buffer washes through;

6. Add running buffer to equilibrate column for sample loading;

7. Add diluted serum sample;

8. Add running buffer to wash unbound protein;

9. Add elution buffer and collect elution fractions for analysis;

10. Acidify each elution fraction.

Please replace the paragraph beginning at page 36, line 2, with the following re-written paragraph:

The instant invention involves the use of a combination of preparatory steps in conjunction with mass spectroscopy and time-of-flight detection procedures to maximize the diversity of biopolymers which are verifiable within a particular sample. The cohort of biopolymers verified within such a sample is then viewed with reference to their ability to evidence at least one particular disease state; thereby enabling a diagnostician to gain the ability to characterize either the presence or absence of [said] at least one disease state relative to recognition of the presence and/or the absence of [said] the biopolymer.